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Amendments to Claims

Claims 1-5 (canceled)

Claim 6. (Currently Amended) An isolated nucleic acid molecule as set forth in SEQ ID NO:18 wherein said nucleic acid molecule encodes *crtE*, *crtX*, *crtY*, *crtI*, *crtB* and *crtZ* or ~~comprising a an isolated nucleic acid molecule polynucleotide~~ having at least 95% identity to SEQ ID NO:18, wherein said isolated nucleic acid molecule polynucleotides encodes the following enzymes : geranylgeranyl pyrophosphate synthase (*crtE*) phytoene synthase (*crtB*), phytoene desaturase (*crtI*) lycopene cyclase (*crtY*), β -carotene hydroxylase (*crtZ*), and zeaxanthin glucosyl transferase, (*crtX*).

Claims 7-13 (Canceled)

Claim 14 (Original). A vector comprising the isolated nucleic acid molecule of Claim 6.

Claim 15 (Canceled)

Claim 16 (Original). A transformed host comprising the isolated nucleic acid molecule of claim 6.

Claim 17 (Previously Presented). The transformed host cell of Claim 16 wherein the host cell is selected from the group consisting of bacteria, yeast, filamentous fungi, algae, and green plants.

Claim 18 (Original). The transformed host cell of Claim 17 wherein the host cell is selected from the group consisting of *Aspergillus*, *Trichoderma*, *Saccharomyces*, *Pichia*, *Candida*, *Hansenula*, *Yarrowia*, *Rhodospiridium*, *Lipomyces*, *Salmonella*, *Bacillus*, *Acinetobacter*, *Zymomonas*, *Agrobacterium*, *Flavobacterium*, *Rhodobacter*, *Rhodococcus*, *Streptomyces*, *Brevibacterium*, *Corynebacteria*, *Mycobacterium*, *Escherichia*, *Pantoea*, *Pseudomonas*, *Methylomonas*, *Methylobacter*, *Methylococcus*, *Methylosinus*, *Methylomicrobium*, *Methylocystis*, *Alcaligenes*, *Synechocystis*, *Synechococcus*, *Anabaena*, *Thiobacillus*, *Methanobacterium*, *Klebsiella*, *Methylophilus*, *Methylobacillus*, *Methylobacterium*, *Hyphomicrobium*, *Xanthobacter*, *Paracoccus*, *Nocardia*, *Arthrobacter*, *Rhodopseudomonas*, *Torulopsis*, *Rhodotorula*, and *Phaffia*.

Claim 19 (Canceled)

Claim 20 (Previously Presented). A method for the production of carotenoid compounds comprising:

- (a) providing a transformed host cell comprising:
 - (i) suitable levels of farnesyl pyrophosphate; and
 - (ii) the isolated nucleic acid molecule of claim 6 under the control of suitable regulatory sequences;
- (b) contacting the host cell of step (a) under suitable growth conditions with an effective amount of a fermentable carbon substrate whereby a carotenoid compound is produced.

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Claim 21 (Previously Presented). A method according to Claim 20 wherein the transformed host cell is selected from the group consisting of C1 metabolizing hosts, bacteria, yeast, filamentous fungi, algae, and green plants.

Claim 22 (Previously Presented). A method according to Claim 21 wherein the C1 metabolizing host is a methanotroph and the fermentable carbon substrate is selected from the group consisting of methane, methanol, formaldehyde, formic acid, methylated amines, methylated thiols, and carbon dioxide.

Claim 23 (Original). A method according to Claim 22 wherein the C1 metabolizing host:

- (a) grows on a C1 carbon substrate selected from the group consisting of methane and methanol; and
- (b) comprises a functional Embden-Meyerhof carbon pathway, said pathway comprising a gene encoding a pyrophosphate-dependent phosphofructokinase enzyme.

Claim 24 (Original). A method according to Claim 23 wherein the C1 metabolizing host cell is a high growth methanotrophic bacterial strain, known as *Methylomonas* 16a and having the ATCC designation PTA 2402.

Claim 25 (Previously Presented). A method according to Claim 20 wherein the transformed host cell is selected from the group consisting of *Aspergillus*, *Trichoderma*, *Saccharomyces*, *Pichia*, *Candida*, *Hansenula*, *Yarrowia*, *Rhodospiridium*, *Lipomyces*, *Salmonella*, *Bacillus*, *Acinetobacter*, *Zymomonas*, *Agrobacterium*, *Flavobacterium*, *Rhodobacter*, *Rhodococcus*, *Streptomyces*, *Brevibacterium*, *Corynebacterla*, *Mycobacterium*, *Escherichia*, *Pantoea*, *Pseudomonas*, *Methylomonas*, *Methylobacter*, *Methylococcus*, *Methylosinus*, *Methylomicrobium*, *Methylocystis*, *Alcaligenes*, *Synechocystis*, *Synechococcus*, *Anabaena*, *Thiobacillus*, *Methanobacterium*, *Klebsiella*, *Methylophilus*, *Methylobacillus*, *Methylobacterium*, *Hyphomicrobium*, *Xanthobacter*, *Paracoccus*, *Nocardia*, *Arthrobacter*, *Rhodopseudomonas*, *Torulopsis*, *Rhodotorula*, and *Phaffia*.

Claim 26 (Previously Presented). A method according to Claim 20, wherein the carotenoid compound produced is selected from the group consisting of, β -carotene, lycopene, poytopene, zeaxanthin and zeaxanthin- β -diglucoside.